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Highlights

- It is proposed that the missing value in a record is handled by utilising the values of the corresponding fields in the k-NNs of this record.
- The proposed method for dealing with missing values allows the use of the traditional blocking techniques to handle the scalability issue.
- The existing Bloom filter protocol has been adapted to address both issues of missing values and privacy preservation

Privacy Preserving Record Linkage in the Presence of Missing Values

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Abstract

The problem of record linkage is to identify records from two datasets, which refer to the same entities (e.g. patients). A particular issue of record linkage is the presence of missing values in records, which has not been fully addressed. Another issue is how privacy and confidentiality can be preserved in the process of record linkage. In this paper, we propose an approach for privacy preserving record linkage in the presence of missing values. For any missing value in a record, our approach imputes the similarity measure between the missing value and the value of the corresponding field in any of the possible matching records from another dataset. We use the k-NNs (k Nearest Neighbours in the same dataset) of the record with the missing value and their distances to the record for similarity imputation. For privacy preservation, our approach uses the Bloom filter protocol in the settings of both standard privacy preserving record linkage without missing values and privacy preserving record linkage with missing values. We have conducted an experimental evaluation using three pairs of synthetic datasets with different rates of missing values. Our experimental results

☆Fully documented templates are available in the elsarticle package on CTAN.

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show the effectiveness and efficiency of our proposed approach.

Keywords: Record linkage, Probabilistic record linkage, Privacy preserving record linkage, Missing values, k-nearest neighbours, Data encryption

1. Introduction

Record linkage, also known as data matching, duplicate detection, or entity resolution, refers to the process of identifying and aggregating records from one or more datasets, which represent the same real-world entities [1, 2]. For example, Table 1 shows two datasets, R and S, which contain the personal information of individuals. To link the two datasets, the desirable output are the record pairs that refer to the same individuals, i.e. $(R2, S1)$.

Record linkage is often needed in tasks such as creating a linked dataset for further analysis [3]. As long as the data for the same entity is spread across more than one dataset, record linkage would be needed for the analysis of such data. For example, in medical and social sciences research, the disjunctive or additional data about the same individual must be obtained by combining two or more different datasets through record linkage, such that complete family trees over a period of time can be created [4].

Unfortunately, records to be linked across different datasets often lack unique identifiers for performing such an identifying and aggregating process [1]. To overcome this problem, many techniques have been developed for record linkage over the past decade [5] in various applications. For example, in the areas of national censuses and health, most of the linkage systems use the probabilistic record linkage technique [6, 7].

Most of the current techniques for record linkage are based on comparing the values of several partially unique fields in a pair of records, which are generally available (e.g. name, date of birth, and address), or even a combination of them to identify and link records about the same individual [5]. However, in various domains, missing values may be present in records due to a variety of reasons. For example, in the case of medical databases, patients may not wish

Table 1: Two example datasets for record linkage.

Dataset	#	*Surname*	*GivenName*	*Gender*	*Street*	*City*	*Postcode*	*Telephone*
R	1	Green	Gabrielle	F	435 s. la cienega blvd.	Los Angeles	92603	426 341 2521
	2	Lorigman	Vinn		8358 sunset blvd. west	Hollywood	92613	421 908 1495
	3		Kte	F	95 ave. a at 6th st.		9261e	427 724 5566
	4	Heron	Keely		3434 peachtree rd.	San Francisco	92692	
	5		Zhane	F		San Francisco	92602	427 939 4314
	6	Hron	David	M	3434 peachtree rd. ne		9260q	
	7	Mulin	Jhane	F		San Francisco	92605	
S	1	Lonkman	Finm		8358 sunset blvd.	W. Hollywood	92612	421-908-1549
	2	Hemmingj	Kade	F	95 ave. a	New York City	92614	427-729-5665
	3	Dixon	Cherea	M	99 e. 52nd st.		9260t	
	4	Heron	Shane	F	3434 peachtree rd.	San Francisco	92602	427-939-4314

to provide all the required information or clinical workflows cannot ensure that data collection and/or documentation are accurate and complete [8]. It was reported that for the electronic medical records of HIV patients, the median missing data rate was about 10.9% [9]. For the problem of missing values in traditional databases for statistical analysis (e.g. statistical classification) [10], a variety of methods have been developed. In general, some of these approaches ignore either the missing values themselves or the records with missing values altogether while the other approaches impute the missing values instead.

Another major challenge in record linkage is how to protect the privacy and confidentiality of sensitive information (e.g. names and addresses of people), when datasets are linked between organisations [2]. In certain applications (e.g. linking large datasets about people), while such personal identifying fields are commonly used in the linkage process, they must be kept private and confidential [11]. The problem of finding records that represent the same individual in separate datasets without revealing the identity of the individual is called privacy-preserving record linkage (PPRL). Although various techniques for PPRL have been developed for linking datasets between organisations, there is currently no work addressing the problem of missing values in record linkage while at the same time addressing the issue of privacy and confidentiality.

In this paper, we propose an approach to record linkage in the presence of missing values, while simultaneously addressing the issue of privacy and confidentiality. For the issue of missing values, our approach imputes the similarity measure between the missing value and the value of the corresponding field in any of the possible matching records in another dataset, using a collection of values for the corresponding field in its k-NNs (Nearest Neighbours) in the same dataset. Our observation is that it is very likely that the record with a missing value and its k-NNs (i.e. very similar records) have similar values for the corresponding field. This observation generally holds in large datasets (e.g. census data). For example, there is a high probability that the people who live in the same address share the same last name or telephone number [12].

The k-NNs of a record with a missing value are selected based on the sim-

ilarity measures between these k-NNs and the record with the missing value. Each of such similarity measures is calculated between the values for each of the corresponding fields in a pair of records, which does not have any missing value. For the values of the corresponding field(s) in the k-NNs, an associated weight vector is constructed, with each weight in the vector representing the distance (i.e. similarity measure) between the respective k-NN and the record with the missing value. These weights will reflect the different levels of contributions that the different values of the corresponding field in the k-NNs make to the imputation of the similarity measure on the corresponding field between the record with the missing value and any of the possible matching records in another dataset.

The reason that a missing value is dealt with in this way, rather than simply taking the value in the 1-NN record as the imputed missing value or deciding on a value by majority voting out of the values in the k-NNs, is to avoid any situation in which the 1-NN record holds a totally different value from the actual missing value, or these records have several slightly different values for the field (e.g. due to typographical errors). For example, as shown in Table 1, for record $R5$ with a missing value of $Surname$, the first of its k-NNs is $R7$, which, however, holds a wrong value of $Surname$ for $R5$, whilst the second and third of its k-NNs and (i.e. $R4$ and $R6$ respectively) hold the correct value of $Surname$ for $R5$.

Our approach uses both the k-NNs of the record with a missing value and the corresponding weight vector of the k-NNs to impute the similarity measure between the missing value and the value of the corresponding field in any of the possible matching records in another dataset. As a result, as long as the majority of the k-NNs of the record with the missing value hold the same value as or similar values (e.g. due to a typographical error) to the actual missing value of the corresponding field, the imputed similarity measure would be reasonable. Since our proposed approach imputes the similarity measure between the values of the same field in two records, traditional blocking techniques [13, 14], which primarily rely on similarity measures on some of the fields in different records,

can be simply applied to address the scalability issue. For privacy preservation, our approach to dealing with missing values enables us to adapt the Bloom filter protocol [15, 16] in our approach to privacy preserving record linkage in the presence of missing values.

This paper makes three novel contributions: First, the missing values in a record are handled by utilising the values of the corresponding fields in the k-NNs of the record. Second, our proposed technique for dealing with missing values allows use of the traditional blocking techniques for dealing with the scalability issue. Finally, we have adapted the Bloom filter protocol in our approach to address both issues of missing values and privacy preservation. The remainder of the paper is organised as follows: Section 2 describes related work. Section 3 presents the formulation of the research problem we solve in this paper and briefly introduces the fundamentals of the techniques proposed for the solutions to the problem. Section 4 describes our proposed approach to privacy preserving record linkage in the presence of missing values. Section 5 presents our experimental evaluation of the proposed approach. Section 6 concludes the paper.

2. Related Work

Record linkage typically uses a set of non-unique identifying fields [17]. Current approaches to record linkage can be divided into three categories. The first category is called deterministic record linkage, in which whether a pair of records match is determined by the exact agreement or disagreement between the corresponding values of each of the identifying fields [18]. The methods of this category have the advantages of being simple, transparent, and easy to accept [18]. However, their common drawback is that they do not tolerate the presence of any errors (e.g. typographical or phonetic errors) in records [8]. The second category are probabilistic record linkage methods, which estimate the likelihood that two records match [8]. They allow the presence of some errors in records by considering the similarity measure between the values of the

corresponding field in the records. The last category of methods are machine learning based, where a variety of machine learning techniques are applied to train a classifier to decide on whether a pair of records matches. Such machine learning approaches can often achieve higher accuracy rates [19].

In some specific domains (e.g. patient records), no private or confidential information can be revealed. As a result, various PPRL techniques have been developed [2]. Although they operate differently, they share the same principle: the records in the datasets to be linked are encoded at the sources while record linkage is carried out based on the encoded records only, such that no sensitive information is ever revealed during the process of record linkage. The existing techniques for PPRL can be generally classified into three generations [2]. The first generation of methods only allow exact matching [20]. They generally encode field values into hash codes, through using some one-way hash functions, and then decide on whether their hash values match in an exact fashion. However, these methods have a major drawback: any small difference (e.g. a difference in a single character) between field values would result in completely different hash values, which makes them only work for exactly matching field values. To overcome this drawback, the second generation of methods use approximate matching. They aim to encrypt records in an appropriate manner such that the similarity measure between the corresponding filed values in a pair of records can be calculated on the basis of their encrypted values [16]. A variety of robust techniques have been developed, for example, Bloom filter protocol [16], phonetic encoding [21], random and public reference values [22], and secure multi-party computation [23]. In addition to approximate matching, the third generation of methods also consider their scalability to large datasets. A number of approaches have been developed by combining existing blocking techniques with some encoding, perturbation, or cryptographic methods [24, 2].

To handle missing values in statistical analysis, there are two major classes of methods: one is simply ignoring the missing values, and the other is estimating the missing values based on the corresponding values of the other records in the same dataset [10]. In the former class, two approaches have been used: either

completely removing the records with missing values or ignoring the fields with missing values in the process of record linkage. However, both approaches may result in valid record pairs being missed, since removing any records or any fields of a record is equivalent to removing data that is originally used for record linkage. In addition, because an eliminated record will never be matched, these methods will always increase the number of non-match record pairs. While for the class of estimation based methods, only rarely have such methods been applied to deal with missing values in record linkage. This is due to the fact that majority of fields in records are strings, the values of which are difficult to impute.

In addition to the statistical approaches to dealing with missing values, machine learning based methods have also been developed, including clustering based techniques [25, 26], autoassociative neural networks [27], decision tree imputation [28] and so on. In particular, the clustering based methods rely on the idea of dividing records in a dataset into clusters, and then replacing the missing values of records in a cluster by some statistical values (e.g. mean or mode values) in the same cluster. There are two different approaches: k-means clustering based and k-NN based. The k-means clustering based imputation methods [26] first apply k-means clustering to divide records into clusters, and then impute the missing values based on the records in a cluster. The k-NN based imputation techniques [25] first decide on the k-NNs of a record with missing values based on a similarity metric, and then use the corresponding values of the k-NNs to impute the missing values in the record.

Recently, three new approaches have been proposed in [8], based on adapting the solutions for dealing with missing values in standard classification to the problem of record linkage with missing values. The first method redistributes field weights associated with the fields with missing values to the other fields, and assigns zero weights to the fields with missing values. The second method imputes the similarity measure between two corresponding fields in a record pair, when either of them has a missing value, rather than imputing the missing value of a field. The last method adds previously considered non-identifying

fields to the set of identifying fields to compensate for the missing values in the existing identifying fields. However, none of the above three methods has either explored solutions to PPRL with missing values or addressed the scalability issue of linking large-scale datasets.

3. Preliminary

Given two datasets, R and S, the problem of record linkage is typically formulated as a classification problem, i.e. whether a pair of records, $(r, s) \in R \times S$, is classified as match, non-match or possible match [6]. A pair of records match if they refer to the same entity (e.g. a patient). The classification algorithm for record linkage uses a similarity vector for each pair of records. Each element in the similarity vector represents the similarity measure between the two corresponding values of an identifying filed in the record pair.

Definition 1 (Similarity Vector). Given t similarity metrics $F = [F_1, F_2, \ldots, F_t]$ and a record pair $(r, s) \in R \times S$, a t-dimensional similarity vector, $f(r, s)$, is defined as $[f_1(r_1, s_1), f_2(r_2, s_2), \ldots, f_t(r_t, s_t)] \in [0, 1]^t$, where $f_i(r_i, s_i)$ $(1 \leq i \leq t)$ represents the similarity measure between the the pair of values in the corresponding fields, $r_i \in r$ and $s_i \in r$, as follows:

$$f_i(r_i, s_i) = \begin{cases} 1 & if\ F_i(r_i, s_i) \geq \gamma_i \\ 0 & otherwise \end{cases} \quad (1)$$

where r_i and s_i are the ith identifying fields of r and s respectively, and γ_i is the threshold for the ith identifying field, which determines the level of similarity measure between r_i and s_i for them to be treated as the same (i.e. the similarity value of 1). For example, given the two datasets R and S shown in Table 1, a string similarity metrics, such as Jaccard distance, can be applied to field *Surname*.

For the linkage of the two datasets shown in Table 1, a record linkage algorithm should return the following classifications: $R2$ and $S1$ is a match; $R3$ and $S2$ as well as $R5$ and $S4$ are possible matches hence require clerical review,

while the other pairs of records are non-matches. Clerical review involves manually determining whether a pair of records matches when it cannot be decided automatically whether such a pair of records match.

Privacy Preserving Record Linkage (PPRL) aims to classify record pairs into two disjoint classes only: matches (M) and non-matches (U). In addition, only the values of those fields in a matching pair of records, which have been agreed between two parties, are revealed. Also, no clerical review is allowed due to privacy. For example, for the two datasets shown in Table 1, a PPRL approach should produce the following output: $R2$ and $S1$ is a match (i.e. in M) with the values of the agreed fields revealed only.

For two large datasets R and S, it is not practical to enumerate all record pairs $(r, s) \in R \times S$, and classify them accordingly. Blocking techniques [13, 14] typically use a blocking scheme to quickly identify a relatively small subset of record pairs, which are more likely to be matched, for the subsequent classification.

Definition 2 (Blocking Scheme). A blocking scheme is defined as a binary function $B : R \times S \rightarrow \{true, false\}$, which has the property that the set of every record pair $(r, s) \in R \times S$, where $B(r, s) = true$, can be computed efficiently.

For example, a blocking scheme could be a string similarity measure between a pair of records on a selected field, such as:

$$Jaccard(r_i, s_i) \geq \theta$$

where $Jaccard$ refers to the Jaccard similarity coefficient, r_i and s_i are the ith fields of the records r and s respectively, while θ is a predefined threshold, where θ can be set to a level so that only the set of record pairs that can be compared in detail efficiently are selected. A more generalised blocking scheme can be defined, which can consist of a combination of similarity measures between two records on one or more selected fields.

3.1. Probabilistic Record Linkage

Probabilistic record linkage is based on the probabilistic decision rule formalised in [6]. It assigns a comparison weight score to a pair of records based on a number of similarity measures between the records on the corresponding fields, and treats a pair of records with a comparison weight score above a given threshold as a match. For a record pair $(r, s) \in R \times S$, a comparison weight score represents the likelihood ratio defined as follows:

$$\mathbb{R}(f(r,s)) = \frac{m(f(r,s))}{u(f(r,s))} \tag{2}$$

where

$$m(f(r,s)) = P(f(r,s) \mid (r,s) \in M) \tag{3}$$

and

$$u(f(r,s)) = P(f(r,s) \mid (r,s) \in U) \tag{4}$$

are the conditional probabilities of $f(r, s)$ given records r and s are a match (i.e. in M) and a non-match (i.e. in U), respectively. Under the assumption of conditional independence [6], both Eqs. (3) and (4) can be simplified as:

$$\begin{aligned} m(f(r,s)) =& m_1(f_1(r_1,s_1)) \times m_2(f_2(r_2,s_2)) \times \ldots \\ & \times m_t(f_t(r_t,s_t)) \end{aligned} \tag{5}$$

and

$$\begin{aligned} u(f(r,s)) =& u_1(f_1(r_1,s_1)) \times u_2(f_2(r_2,s_2)) \times \ldots \\ & \times u_t(f_t(r_t,s_t)) \end{aligned} \tag{6}$$

where for $i = 1, 2, \ldots, t$

$$m_i(f_i(r_i,s_i)) = P(f_i(r_i,s_i) \mid (r,s) \in M) \tag{7}$$

and

$$u_i(f_i(r_i,s_i)) = P(f_i(r_i,s_i) \mid (r,s) \in U) \tag{8}$$

are the conditional probabilities of $f_i(r_i, s_i)$, given records r and s are a match (i.e. in M) and non-match (i.e. in U), respectively. To further simplify the

computation of the likelihood ratio in Eq. (2), a computationally convenient function $\log_2$ is used, such that an increase of 1 unit in $\log_2 \mathbb{R}(f(r,s))$ corresponds to an increase of 2 units in $\mathbb{R}(f(r,s))$. Therefore, the comparison weight score for a pair of records r and s can be expressed as:

$$\begin{aligned}\mathbb{W}(f(r,s)) =& \log_2 \frac{m(f(r,s))}{u(f(r,s))} \\ =& \mathbb{W}_1(f_1(r_1,s_1)) + \mathbb{W}_2(f(r_2,s_2)) + \dots \\ &+ \mathbb{W}_t(f_t(r_t,s_t))\end{aligned} \tag{9}$$

where $\mathbb{W}_i(f_i(r_i,s_i))$ $(i = 1,2,\dots,t)$ is the comparison weight score for the ith identifying fields of r and s, obtained as follows:

$$\mathbb{W}_i(f_i(r_i,s_i)) = \begin{cases} \mathbb{W}_i^a & if\ f_i(r_i,s_i) = 1 \\ \mathbb{W}_i^d & if\ f_i(r_i,s_i) = 0 \end{cases} \tag{10}$$

where $\mathbb{W}_i^a$ and $\mathbb{W}_i^d$ are the agreement and disagreement weights for the ith identifying field respectively, calculated as follows:

$$\mathbb{W}_i^a = \log_2 \left(\frac{m_i(f_i(r_i,s_i) = 1)}{u_i(f_i(r_i,s_i) = 1)} \right) \tag{11}$$

and

$$\mathbb{W}_i^d = \log_2 \left(\frac{1 - m_i(f_i(r_i,s_i) = 1)}{1 - u_i(f_i(r_i,s_i) = 1)} \right) \tag{12}$$

respectively. Both $m_i(f_i(r_i,s_i))$ and $u_i(f_i(r_i,s_i))$ $(i = 1,2,\dots,t)$ can be estimated either using a given training dataset or by the EM algorithm as described in [29]. Finally, whether a pair of records r and s is a match or non-match is classified as follows:

$$(r,s) = \begin{cases} \text{match} & if\ \mathbb{W}(f(r,s)) \geq \lambda \\ \text{non-match} & otherwise \end{cases} \tag{13}$$

where λ is a pre-defined threshold, and its value can be obtained by balancing between an acceptable recall and precision.

3.2. Bloom Filter Protocol

The Bloom filter protocol has been proposed for encryption in record linkage [16]. Under this protocol, the dataset owners involving in the linkage process

should first agree on: A bit array of length l, in which every bit is initially set to 0, and m independent hash functions $\{h_1, h_2, \ldots, h_m\}$, each of which should be one way only, such that it is impossible to determine the original input from a hash output. In addition, each hash function should always generate the same output for the same input. An input x is encrypted by each of the hash functions h_p $(p = 1, 2, \ldots, m)$, which produces an output $h_p(x)$. In order to store each output $h_p(x)$ in a shared Bloom filter with fixed length l, the remainder q of the division of the output $h_p(x)$ by the length of Bloom filter l is obtained by the modulo operation, mod, as:

$$q = h_p(x) \bmod l \tag{14}$$

where $0 \leq q \leq l - 1$. Then, the $(q + 1)$th bit in the Bloom filter is set to 1. As a result, for each output $h_p(x)$, there is always a bit in the Bloom filter to be set to 1. To reduce the possibility that two different input values x and y are mapped onto the same bit in a Bloom filter, each input value is hashed m times by m hash functions (i.e. by setting a large number for m), so that it is more likely that each hash output uniquely corresponds to a bit in the Bloom filter. If the corresponding bit has already been set to 1, no change is made.

The similarity measure between two input values can therefore be compared in a privacy preserving manner once they are mapped onto two respective Bloom filters. The similarity measure between two Bloom filters can be calculated using Dice coefficient as follows:

$$F^{DC}(\mathbb{B}(r_i), \mathbb{B}(s_i)) = \frac{2 \times n_{\mathbb{B}(r_i)\mathbb{B}(s_i)}}{n_{\mathbb{B}}(r_i) + n_{\mathbb{B}}(s_i)} \tag{15}$$

where $\mathbb{B}(r_i)$ and $\mathbb{B}(s_i)$ are the Bloom filters of the values for the ith identifying fields of records r and s respectively, $n_{\mathbb{B}(r_i)\mathbb{B}(s_i)}$ represents the number of the corresponding bits in both Bloom filters $\mathbb{B}(r_i)$ and $\mathbb{B}(s_i)$, which have been set to 1, while $n_{\mathbb{B}}(r_i)$ and $n_{\mathbb{B}}(s_i)$ represents the number of bits in Bloom filters $\mathbb{B}(r_i)$ and $\mathbb{B}(s_i)$ respectively, which have been set to 1.

Dice coefficient is the most common way of measuring the similarity between two Bloom filters. Compared to token-based similarity metrics (e.g. Jaccard

index, overlap coefficient, and Hamming distance), Dice coefficient is insensitive to the number of 0 bits in Bloom filters. In addition, it has been reported [15] that Dice coefficient is more suitable for large-scale record linkage, compared to an alternate metric for comparing Bloom filters (i.e. secure edit distance [30]). Secure edit distance [30] is computationally more expensive as it requires a specific way of creating Bloom filters and the password used to encrypt data needs to be known to the third party.

We now illustrate an example of encryption using the Bloom filter protocol. We need to calculate the similarity measure between $r_i = SMITH$ and $s_i = SMYTH$ in a privacy preserving manner. As shown in Table 2, we assume that the length of Bloom filter l and the number of independent hash functions m are set to 100 and 3, respectively. The output of each of the independent hash functions $h_p(x)$ $(p = 1, \ldots, m)$ can be efficiently computed on the basis of two independent hash functions $\hat{h}_1$ and $\hat{h}_2$ [31], as:

$$h_p(x) = \hat{h}_1(x) + p\hat{h}_2(x) \tag{16}$$

In this example, we use two well known cryptographic hash functions SHA1 and MD5 for $\hat{h}_1$ and $\hat{h}_2$, respectively. As we can see in Table 2, 13 bits are set to 1 in both $\mathbb{B}(r_i)$ and $\mathbb{B}(s_i)$, and 17 bits are set to 1 in $\mathbb{B}(r_i)$ while 16 bits are set to 1 in $\mathbb{B}(s_i)$. Using Dice coefficient, the similarity measure between $\mathbb{B}(s_i)$ and $\mathbb{B}(r_i)$ can be calculated as follows:

$$\begin{aligned} F^{DC}(\mathbb{B}(r_i), \mathbb{B}(s_i)) &= \frac{2 \times n_{\mathbb{B}(r_i)\mathbb{B}(s_i)}}{n_{\mathbb{B}}(r_i) + n_{\mathbb{B}}(s_i)} \\ &= \frac{2 \times 13}{16 + 17} \\ &\approx 0.788 \end{aligned} \tag{17}$$

4. Proposed Approach

In this section, we first describe a k-NN based approach for dealing with missing values in the standard probabilistic record linkage setting. We then de-

scribe how such an approach can be used in the probabilistic privacy preserving record linkage in the presence of missing values.

4.1. A k-NN Based Approach to Probabilistic Record Linkage in the Presence of Missing Values

For each record in a dataset with a missing value in any of its identifying fields, we first find a set of records in the same dataset, which are the k-NNs of the record. This set of records will then be used to impute the similarity measure between the missing value and a value of the corresponding field in any of the possible matching records in another dataset.

4.1.1. k-NN Graph Construction

Given each record in a dataset, we first generate a k-NNG (Nearest Neighbour Graph) in which a node represents the record, k other nodes represent k records in the same dataset, which are most similar to the given record by a given similarity measure, with each of the k nodes connected to the node for the given record.

The naive way of generating all the k-NNGs for all the records in a large dataset is computationally expensive[32]. As a result, much research has been focused on generating k-NNGs in an efficient manner [33]. For example, techniques have been proposed for generating exact k-NNGs [34], and approximate k-NNGs using space partition trees [35, 36], local search [37] and locality sensitive hashing [38]. In record linkage, blocking techniques [24] have been proposed for reducing the number of record pairs to be compared. In particular, those blocking techniques, referred as intra-blocking schemes can be used to split a dataset into non-overlapping blocks, where records within the same block are more similar to each other than to those in a different block. For a record with a missing value, we find its k-NNs in the same block.

An intra-blocking scheme is based on comparing either the values of a single record field, or the concatenation of values from several record fields. As a result, an intra-blocking scheme would require at most $n_t \times (n_t - 1)/2$ computations,

which corresponds to a computational complexity of $O(n_t^2/2)$, where n_t refers to the total number of records in a dataset. Usually, such a scheme is chosen to be cheap to operate, so that it can be run in a reasonable time for moderately sized datasets [39]. For an intra-blocking scheme, if there is any missing value in the record field(s) for intra-blocking, it would ignore the missing value and simply return a $false$.

Given a t-dimensional similarity metrics $\rho = [\rho_1, \rho_2, \ldots, \rho_t]$ for t identifying fields, for each record in a dataset R with a missing value in any of its identifying fields, we need to calculate the similarity measure between the given record and each of the other records in R in order to find the k-NNs of the given record.

We use the probabilistic record linkage framework described in Section 3.1. For a pair of records r^a and r^b in the same dataset, its comparison weight score $\mathbb{W}^\rho(\rho(r^a, r^b))$ can be calculated as:

$$\begin{aligned}\mathbb{W}^\rho(\rho(r^a, r^b)) =& \mathbb{W}_1^\rho(\rho_1(r_1^a, r_1^b)) + \mathbb{W}_2^\rho(\rho_2(r_2^a, r_2^b)) + \ldots \\ &+ \mathbb{W}_t^\rho(\rho_t(r_t^a, r_t^b))\end{aligned} \tag{18}$$

where $[r_1^a, r_2^a, \ldots, r_t^a]$ and $[r_1^b, r_2^b, \ldots, r_t^b]$ are the t-dimensional vectors of records r^a and r^b. If there is a missing value of any identifying field in either $[r_1^a, r_2^a, \ldots, r_t^a]$ or $[r_1^b, r_2^b, \ldots, r_t^b]$, we set $\rho_i(r_i^a, r_i^b) = 0$, for $i = 1, 2, \ldots, t$.

Finally we set a threshold, ε, so that only those records that have a comparison weight score above the threshold are selected and ranked as the possible k-NNs of the record. Formally, a record r^c is labelled as a k-NN of record r^a, if $\mathbb{W}^\rho(\rho(r^a, r^c)) \geq \varepsilon$ and r^c is among the k-NNs of r^a. The pseudocode for finding the k-NNs of a record with a missing value is presented in Algorithm 1.

In Algorithm 1, there are two iterations: the main part of the computational cost is in the first iteration where the comparison weight score between the record with a missing value and each of the other records in the same dataset is calculated. The second iteration involves filtering through a set of similarity measures with a pre-defined threshold only to select the set of k-NNs. The total computational complexity is in the order of $O(n_k \times t)$, where n_k is the number of records in the same block, and t is the dimensionality of the record vector.

Algorithm 1 Finding the k-NNs of a record with a missing value

Input: record r^u, n_k records $\{r^{v_1}, r^{v_2}, \ldots, r^{v_n}\}$ in the same block of r^u, number of k-NNs k, threshold ε

Output: k-NN set K^u

$G \leftarrow \emptyset$
$K^u \leftarrow \emptyset$
for $i = 1$ to n_k **do**
  Compute $\mathbb{W}^\rho(\rho(r^u, r^{v_i}))$ with (18)
  $G \leftarrow G \cup \{\mathbb{W}^\rho(\rho(r^u, r^{v_i}))\}$
end for
Select k records in G, $\{r^{k_1}, r^{k_2}, \ldots, r^{k_k}\}$
for $i = 1$ to k **do**
  if $\mathbb{W}^\rho(\rho(r^u, r^{k_i})) \geq \varepsilon$ **then**
    $K^u \leftarrow K^u \cup \{r^{k_i}\}$
  end if
end for
return K^u

4.1.2. Calculating Weights of k-NNs

We generate a weight vector for the k-NNs of each record with a missing value. Each element in the weight vector is assigned on the basis of the comparison weight score between the given record and each of its corresponding k-NNs. Given a record r^u in dataset R, and its k-NNs $K^u = \{r^{k_1}, r^{k_2}, \ldots, r^{k_k}\}$ in R, the corresponding weight vector w^u is computed as follows:

$$w^u = [\mathbb{W}^\rho(\rho(r^u, r^{k_1})), \mathbb{W}^\rho(\rho(r^u, r^{k_2})), \ldots, \mathbb{W}^\rho(\rho(r^u, r^{k_k}))] \tag{19}$$

where $\mathbb{W}^\rho(\rho(\cdot, \cdot))$ is the comparison weight score calculated using Eq. (18). Furthermore, the weight vector w is normalised to a unit vector $\overline{w^u}$, as:

$$\overline{w^u} = \frac{w^u}{\|w^u\|_2} \tag{20}$$

where $\|w^u\|_2$ is the 2-norm of w^u and computed as:

$$\|w^u\|_2 = \sqrt{\sum_{i=1}^{k} \mathbb{W}^{\rho}(\rho(r^u, r^{k_i}))^2} \tag{21}$$

4.1.3. Dealing with Missing Values in Record Pairs

In order to classify a pair of records as match or non-match, the classifier needs to take as input a similarity vector for the pair. Each element in the similarity vector represents the similarity measure between the values of the two corresponding identifying fields in the records. However, when either of the values is missing, instead of imputing the missing value, we impute the similarity measure using the k-NNs of the record with the missing value. The similarity measure $F_i(r_i, s_i)$ on the ith identifying fields of records r and s, when either of the identifying fields has a missing value, is computed as follows:

$$F_i(r_i, s_i) = \begin{cases} F_i(\sim, s_i) & \text{if } r_i \text{ has a missing value} \\ F_i(r_i, \sim) & \text{if } s_i \text{ has a missing value} \\ 0 & \text{if both } r_i \text{ and } s_i \text{ have missing values} \end{cases} \tag{22}$$

where $F_i(\sim, s_i)$ represents the imputed similarity measure given r_i has a missing value, calculated as follows:

$$\begin{aligned} F_i(\sim, s_i) =& F_i(r_i^{x_1}, s_i) \times \overline{w^{x_1}} + F_i(r_i^{x_2}, s_i) \times \overline{w^{x_2}} + \dots \\ &+ F_i(r_i^{x_k}, s_i) \times \overline{w^{x_k}} \end{aligned} \tag{23}$$

where $\{r^{x_1}, r^{x_2}, \dots, r^{x_k}\}$ are the k values of the ith identifying fields in the k-NNs of the record r, and $\overline{w^x} = [\ \overline{w^{x_1}}, \overline{w^{x_2}}, \dots, \overline{w^{x_k}}\ ]$ is the corresponding weight vector of the k-NNs.

Similarly, $F_i(r_i, \sim)$ represents the imputed similarity measure given s_i has a missing value, calculated as follows:

$$\begin{aligned} F_i(r_i, \sim) =& F_i(r_i, s_i^{y_1}) \times \overline{w^{y_1}} + F_i(r_i, s_i^{y_2}) \times \overline{w^{y_2}} + \dots \\ &+ F_i(r_i, s_i^{y_k}) \times \overline{w^{y_k}} \end{aligned} \tag{24}$$

where $\{s^{y_1}, s^{y_2}, \ldots, s^{y_k}\}$ are the k values of the i identifying fields in the k-NNs of record s, and $\overline{w^y} = [\ \overline{w^{y_1}}, \overline{w^{y_2}}, \ldots, \overline{w^{y_k}}\ ]$ is the corresponding weight vector of the k-NNs.

To illustrate, assume that the similarity measure between the ith identifying fields r_i and s_i (e.g. $r_i = SMITH$ and $s_i = SMYTH$) of the records r and s needs to be computed. We assume that an appropriate similarity metrics can be used for measuring the similarity between the ith fields in the records. For purpose of illustration, we use the combination of 2-gram (i.e. bigram) and Dice coefficient. It has been shown in [40] that using the combination of 2-gram (i.e. bigram) and Dice coefficient could achieve a higher accuracy rate, compared to other string similarity measures. Using the 2-gram technique, each of r_i and s_i is split into a set of two adjacent letters, with blanks first padded on both sides of the string to make the first and last letters their own bigrams (i.e. $\{\_S, SM, MI, IT, TH, H\_\}$ and $\{\_S, SM, MY, YT, TH, H\_\}$ for r_i and s_i, respectively). In both bigrams of r_i and s_i, there are 6 members, 4 of which are in common. The Dice coefficient between r_i and s_i is:

$$\begin{aligned} F^{DC}(r_i, s_i) &= \frac{2 \times n_{r_i s_i}}{n_{r_i} + n_{s_i}} \\ &= \frac{2 \times 4}{6 + 6} \\ &\approx 0.667 \end{aligned} \tag{25}$$

The value of Dice coefficient ranges between 0 and 1, with a higher value representing a higher degree of similarity. Assume that we still have $r_i = SMITH$ but the value of s_i is missing. In this case, we have three values SMY and two $SMYTH$s that are the corresponding values of the ith identifying fields in the 3-NNs of record s, along with their corresponding weight vector $\bar{w} = [0.35, 0.33, 0.32]$. First, we would need to generate three corresponding bigram sets for the three different values (i.e. $SMITH$, SMY and $SMYTH$): $\{\_S, SM, MI, IT, TH, H\_\}$, $\{\_S, SM, MY, Y\_\}$ and $\{\_S, SM, MY, YT, TH, H\_\}$, respectively. It can be seen that there are 6 and 4 members in the bi-gram sets of $SMITH$ and SMY respectively, 2 of which are in common. Then, using the

same similarity metrics (i.e. Dice coefficient), we can impute the similarity measure between r_i and s_i with SMY, the two $SMYTH$, and their corresponding weights as follows:

$$F^{DC}(r_i, \sim) = \frac{2 \times 2}{6+4} \times 0.35 + \frac{2 \times 4}{6+6} \times (0.33 + 0.32)$$
$$\approx 0.573 \tag{26}$$

It can be seen that the difference between the similarity values calculated using Eqs. (25) and (26) is fairly small, which shows the promise of the proposed approach for imputing similarity measures.

4.2. Privacy Preserving Record Linkage with Missing Values

Privacy Preserving Record Linkage (PPRL) requires that the fields about personal information in each of the two datasets to be encrypted by their corresponding owner: First, the two owners agree on a password or pass phrase for the purpose of encryption; Then they encrypt these fields using an encryption software; Finally, the encrypted fields are used as encrypted identifying fields for record linkage.

4.2.1. Privacy Preservation in the Presence of Missing Values

In order to deal with missing values in privacy preserving record linkage, we propose to adapt the Bloom filter approach to PPRL developed in [16]. There are several reasons why we have chosen to adapt this approach over other methods for privacy preserving record linkage in the presence of missing values. First, the Bloom filter approach allows the similarity measure between the two values of the corresponding identifying fields in two records to be calculated even after the two values have been encrypted, which is required in probabilistic record linkage. Second, it has shown quality improvements over other privacy preserving protocols [16] like the Swiss anonymous linkage code [41], which implements an identifier based on the phonetic codes of some identifying fields. Third, it appears robust, well-developed, and adaptable for large-scale record linkage [15]. Finally, and most importantly, the Bloom filter approach can be

easily adapted to work with the k-NNs of a record with a missing value and the weight vector of the k-NNs.

The Bloom filter approach to PPRL [16] uses a three-party protocol, where the linkage is done by a (trusted) third party (i.e. the linkage unit) in a Honest-But-Curious (HBC) model [2]. The two dataset owners encrypt their data records, and transfer the encrypted data securely to the linkage unit. The HBC model assumes that each of the three parties correctly follows the protocol, while being curious about whether they are able to find out as much information as possible from any received data [3]. The Bloom filter approach [16] can stop any dictionary attack as long as the third-party linkage unit does not collude with either of the dataset owners. Although there are still some other types of potential attacks (e.g. frequency attacks), a number of additions to the original Bloom filter approach have enhanced its level of security [42]. For each record with a missing value, we need to encrypt the values of the corresponding identifying fields in the k-NNs of the record, along with their weight vector. We propose a method to encrypt each of these values onto a Bloom filter, along with the weight of the corresponding NN. To achieve this, instead of simply setting the bit in the Bloom filter, which corresponds to the hash output of the bigram set of such a value, to 1, it is set to the weight of the corresponding NN. When the hash output of more than one bigram set is mapped to the same bit in the Bloom filter, the bit is set to the sum of all the corresponding weights.

In the previous example, we have $r_i = SMITH$ in record r while the value of s_i is missing in record s. We also have three values SMY and two $SMYTH$s that are the corresponding values of the ith identifying fields in the 3-NNs of record s, along with their weight vector $\bar{w} = [0.35, 0.33, 0.32]$. We now need to map the bigrams of these three values onto two separate Bloom filers: one for $SMITH$, while the other for both SMY and two $SMYTH$. We can then calculate the Dice coefficient between the two Bloom filers, which imputes the similarity measure between $r_i = SMITH$ and s_i with a missing value. Since we now have real numbers instead of binary numbers in the Bloom filer for SMY and the two $SMYTH$, the original Dice coefficient formula as shown in Eq.

(15) needs to be adapted as follows:

$$\hat{F}^{DC}(\mathbb{B}(r_i), \mathbb{B}(s_i)) = \frac{2 \times \text{sum}(\mathbb{B}(r_i) \cdot \mathbb{B}(s_i))}{\text{sum}(\mathbb{B}(r_i)) + \text{sum}(\mathbb{B}(s_i))} \tag{27}$$

where the two Bloom filers $\mathbb{B}(r_i)$ and $\mathbb{B}(s_i)$ are treated as vectors, and $\cdot$ represents the dot product, and $\text{sum}(\cdot)$ corresponds to the sum of every value in a vector. It can be seen that, for two Bloom filters with binary values, the original Dice coefficient formula (as in Eq. (15)) is a special case of the adapted Dice coefficient formula (as in Eq. (27)).

With the Bloom filter length l set to the exactly same as before, and the bigrams in Table 2, the calculation of the Dice coefficient between $r_i = SMITH$ and s_i with a missing value is done in a privacy preserving manner, as follows:

$$\begin{aligned}
\hat{F}^{DC}(\mathbb{B}(r_i), \mathbb{B}(\sim)) &= \frac{2 \times \text{sum}(\mathbb{B}(r_i) \cdot \mathbb{B}(\sim))}{\text{sum}(\mathbb{B}(r_i)) + \text{sum}(\mathbb{B}(\sim))} \\
&= \frac{2 \times (0.65 + 1 \times 4 + 0.65 \times 3 + 1 \times 3 + 0.65 + 1)}{17 + 14.250} \\
&= \frac{2 \times 11.250}{17 + 14.250} \\
&= 0.720
\end{aligned} \tag{28}$$

where the Bloom filter $\mathbb{B}(\sim)$ is calculated with SMY, and $SMYTH$s, along with the weight vector $\bar{w}$ of the corresponding 3-NNs, as shown in the last column of Table 2. Again, comparing the similarity measures calculated by Dice coefficient in Eqs. (17) and (28), we can see that the difference between the two measures is also fairly small. This shows that the proposed approach for dealing with missing values can work well in the context of privacy preserving record linkage using the Bloom filter protocol.

4.2.2. Computational Complexity

In this section, we analyse the computational complexity of different stages of our proposed approach to privacy preserving record linkage in the presence of missing values. Our approach starts with the intra-blocking process in each of the datasets R and S. Assume that the numbers of records in R and S are n_R and n_S, and their corresponding numbers of missing values are m_R and m_S.

For the two intra-blocking processes in R and S respectively, the corresponding computational complexities are $O(n_R^2/2)$ and $O(n_S^2/2)$, respectively. In the next stage, our approach searches for the k-NNs of each record with missing values in the same block. For both datasets, R and S, this search process has the computational complexity of $O((m_R + m_S) \times n_{kA} \times t)$, where n_{kA} refers to the average number of records within each block, and t is the dimensionality of the record vector. For the next imputation process, the corresponding computational complexity would be $O((m_R + m_S) \times k \times l)$, where k corresponds to k-NN and l is the length of the Bloom filter. For the following blocking process, it would require a hash operation with a complexity of $O((n_R + n_S) \times q_B \times p)$, a communication cost with a complexity of $O((n_R + n_S) \times l)$, and a bit comparison with a complexity of $O(n_R \times n_S \times l^2)$, where q_B is the average number of n-grams in each record field for blocking, and p is the number of hash functions used to map n-grams into a Bloom filter. For the final matching stage, there would be another hash operation with a complexity of $O(n_B \times (n_{RL} + n_{SL}) \times q_L \times p)$, another communication cost with a complexity of $O(n_B \times (n_{RL} + n_{SL}) \times l)$, and another bit comparison with a complexity of $O(n_B \times n_{RM} \times n_{SM} \times l^2)$, where n_B refers to the number of blocks after blocking, n_{RL} and n_{SL} represent the average number of records in each block from R and S respectively, q_L is the average number of n-grams in each record field for linkage, and n_{RM} and n_{SM} correspond to the maximum numbers of records in each block from R and S respectively.

5. Experimental Evaluation

In this section, we present the experimental results of our proposed approach. We have compared our approach with five existing algorithms for record linkage in both the absence (i.e. PRL and BF) and presence (i.e. FRIL-0, FRIL-100 and FLE) of missing values: the standard Probabilistic Record Linkage (PRL) method [6], the Bloom Filter (BF) approach [15, 16], the two methods available in the Fine-grained Record Integration and Linkage (FRIL) tool FRIL-0 and

FRIL-100 [43], as well as the Full Linkage Expansion (FLE) technique proposed in [8]. We conducted all the experiments using MATLAB R2014b on a machine with 3.6-GHz Intel Core i7 CPU and 16-GB DDR3 RAM running the Windows 7 operating system. The objective of our evaluation is to show that our proposed method outperforms the three existing techniques (i.e. FRIL-0, FRIL-100, and FLE) for record linkage in the presence of missing values, while the other two existing methods (PRL and BF) are used as the baselines for standard record linkage and privacy preserving recording linkage without missing values.

5.1. Datasets

For both algorithms PRL and BF, there is no missing value in the datasets for evaluation. For the other three algorithms FRIL-0, FRIL-100 and FLE, as well as our proposed approach, there are a certain percentage of missing values in the datasets. We have generated and used a collection of synthetic datasets based on GeCo [44, 45]. There are several benefits from choosing synthetic datasets over real ones: First, the dataset size can be set with a computational cost estimate. Second, we can define the record fields in the dataset. For example, for our experimental evaluation, we have chosen six fields (i.e. $GivenName$, $Surname$, $Postcode$, $Telephone$, $Gender$, and $City$) for linkage. These are often available in real datasets. Third, the ground truth of the record linkage results is known, to facilitate the quality assessment for benchmarking. Finally, the percentage of missing values in datasets can be controlled, such that benchmarking can be carried out at different levels. Each pair of synthetic datasets consists of two individual datasets, R and S, as well as the two corresponding datasets R' and S' with a certain percentage of missing values. Table 3 shows the characteristics of datasets R and S, including the sizes (i.e. the number of records), the first six fields used as identifying fields, the similarity metrics used for each of the six identifying fields, the blocking and intra-blocking schemes used. There is also an additional 7th ID field in the datasets for the purpose of labelling matching pairs of records only. For brevity, the names of the first six fields are abbreviated by their first letters.

20% of the records in datasets R and S are the same (i.e. those records with the same IDs in both datasets). To simulate various types of errors (e.g. typographical errors) in records to reflect the quality of typical linked datasets, a variety of the corruption methods in GeCo [44, 45] have been used (e.g. phonetic variation, keyboard mistake, name misspelling), to randomly corrupt any four of the first six fields of each record. Each pair of datasets R' and S' have been generated from the same pair of datasets R and S respectively with a certain percentage of records in R' and S' with a missing value in one of the first six fields. To generalise the characteristics of synthetic datasets, three pairs of synthetic datasets R and S have been generated, along with three pairs of R' and S' with missing values, which have 10%, 20%, and 25% of records with missing values. We have used two similarity metrics (i.e. Dice coefficient ($\mathbb{DC}$) and string equality ($\mathbb{SE}$)) for calculating the similarity measures between the corresponding values for each of the first six fields, as shown in Table 3. Both similarity metrics can be computed efficiently [1]. In Table 3, for example, $\mathbb{DC}(GN)$ denotes that Dice coefficient has been used on field $GivenName$, and $\mathbb{DC}(P, C)$ denotes that Dice coefficient has been used on the concatenation of fields $Postcode$ and $City$.

5.2. Algorithms

PRL and BF are the two algorithms for standard record linkage and privacy preserving record linkage respectively. We run them on the three pairs of datasets R and S respectively, to benchmark the performances of standard record linkage and privacy preserving record linkage on each pair of datasets. FRIL-0 and FRIL-100 are two of the existing algorithms for record linkage with missing values: FRIL-0 assumes that each of the missing values is completely different from the value of the corresponding field in the matching record from another dataset (i.e. the similarity measure for the corresponding field in the similarity vector is 0). In contrast, FRIL-100 assumes that each of the missing values is identical to the value of the corresponding field in the matching record from another dataset (i.e. the similarity measure for the corresponding field in

the similarity vector is 1). FLE is one of the three algorithms proposed in [8] for record linkage with missing values, which is reported to have achieved the best performance among the three algorithms. For a record with missing values, FLE first redistributes the weights associated with the fields with missing values to the other fields without missing values, where the weight redistribution is based on relative proportions across the remaining fields; It then assigns zero weight to those fields with missing values. We have run FRIL-0, FRIL-100 and FLE for record linkage with missing values on each pair of datasets R' and S' to benchmark the performance of record linkage with missing values. Their performances have been compared with the performances of our algorithms for privacy preserving record linkage with missing values.

5.3. Evaluation

For the PRL, FRIL-0, FRIL-100 and FLE algorithms, no field in the datasets was encrypted. For the algorithm BF and our algorithm for privacy preserving record linkage with missing values, all the fields in the datasets that contain personal information were encrypted using the Bloom filter protocol. The similarity measure for each of the fields in the similarity vector for each pair of records was calculated using a combination of bigrams and Dice coefficient. For encryption using the Bloom filter protocol, the implementation described in [16] was used for creating Bloom filters with some adaptations: the length of the Bloom filters l and the number of independent hash functions m were set to 100 and 3, respectively. The settings were set the same as for the method in [15], with the same ratio of l to m as in [16] (i.e. the ratios of l to m set to 1000 and 30, respectively). Although these settings may result in a slightly higher false positive rate, compared to those in [16], they helped dramatically reduce the sizes of the Bloom filters while achieving the same performance.

For each pair of datasets, the performances of the five existing algorithms PRL, FRIL-0, FRIL-100, FLE and BF were compared with the performances of our own algorithms respectively. In all the existing algorithms and our own algorithms, we used the probabilistic record linkage framework, where the agree-

ment and disagreement weights were calculated using the EM method described in [29]. The performances of each algorithm with different thresholds were measured, with the highest performance used for comparison.

Two blocking schemes, as shown in Table 3, were used for blocking: one is Dice coefficient between the bigrams of the concatenation *Surname* and the first initial of *GivenName*, and the other is Dice coefficient between the special bigrams of *Telephone*. Since the values of field *Telephone* are in numeric string format, the order of occurrences of individual digits needs to be kept. In addition, there are smaller variations among different string positions (i.e. digits are from 0 to 9 only), which makes the standard bigram technique less effective for distinguishing them from each other. To tolerate small typographical errors in *Telephone* (e.g. due to typing errors), special n-grams were generated for *Telephone*. The special n-grams of a string are the combinations of individual n-grams of the string and the order of their occurrences. For example, for a value 1234567 of *Telephone*, its special 2-gram set is $\{112, 223, 334, 445, 556, 667\}$ (with the first digits in each bigram indicating its order). Similarly, three intra-blocking schemes, as shown in Table 3, were defined for the efficient search of the k-NNs of a record with a missing value in a dataset.

5.4. Linkage Results

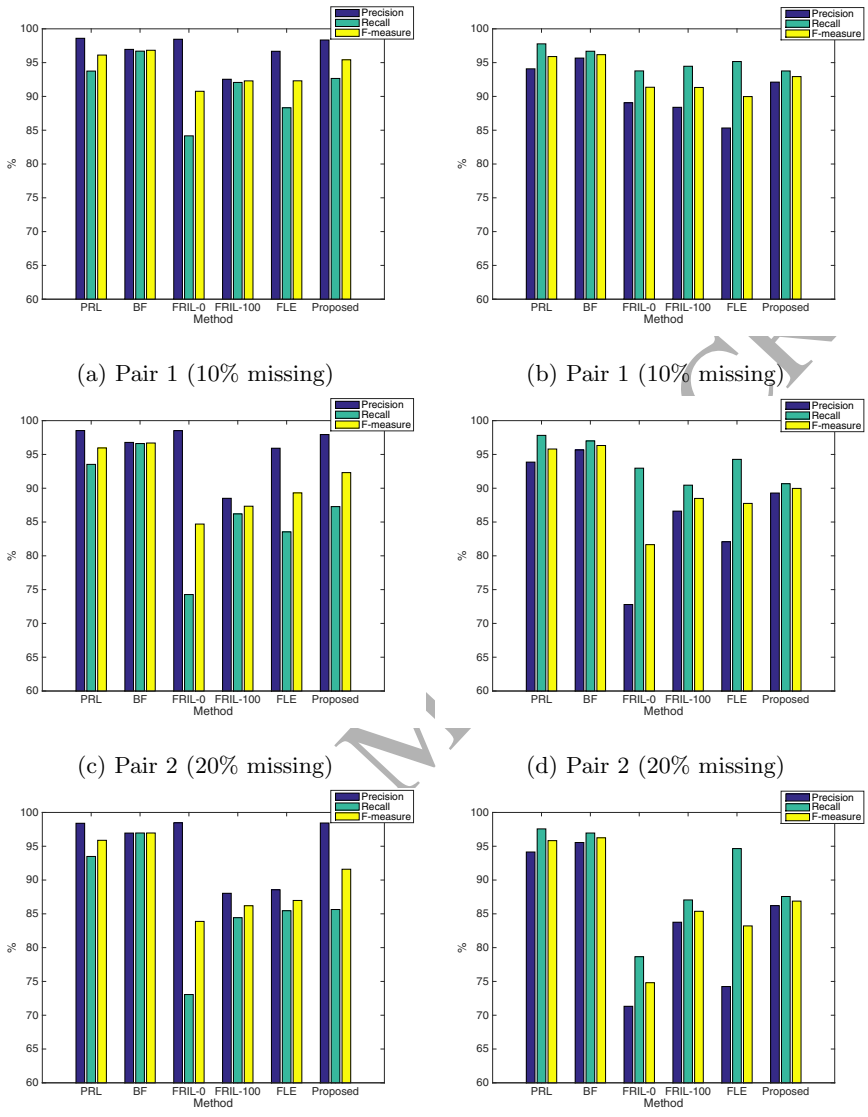
Figure 1 shows the comparison of performances across different algorithms. In each of the subfigures, a vertical dashed line is used to separate those algorithms that do not deal with missing values and the other algorithms that deal with missing values. The quality of each record linkage algorithm was evaluated on precision, recall and F-measure respectively. F-measure is the harmonic mean of precision and recall. For each of the six algorithms, a threshold λ for determining whether a pair of records is a match or non-match was set to the level that maximised the corresponding F-measure. As shown in Figure 1, for the three different rates of missing values, our algorithm outperforms both FRIL-100 and FLE on both precision and recall. Though the precision of our algorithm is slightly lower than that of FRIL-0, FRIL-0 takes the most cautious approach

by assuming that a missing value is completely different from the value of the corresponding field in the matching record from another dataset (i.e. similarity measure is 0). On the other hand, our algorithm does not have this assumption, hence handling missing values better. Compared with the other two algorithms PRL and BF, our algorithm achieved a similar precision but a lower recall. This was because that some records with missing values in the datasets do not have any k-NNs or some of their k-NNs also have missing values in the same fields. As the rate of missing values increases, the recall of our algorithms decrease.

To show that our proposed approach works well with the traditional blocking techniques to address the scalability issue in record linkage, the percentages of record pairs (to be matched) rejected and true matches retained after blocking by each of the six methods for three different rates of missing values are shown in Figures 2 and 3, respectively. It can be seen that our proposed approach outperformed the other three algorithms for record linkage with missing values, especially at a higher rate of missing values. This is because that the proposed approach imputes similarity measures between two records on the fields with missing values, which can then be used for blocking.

5.5. Computational Costs

To show the scalability of the proposed approach, the runtime of each of the methods on each of the datasets was recorded to produce the average runtimes, as shown in Table 4. All the six methods were run independently in Matlab: for both the proposed method and BF, the similarity calculation was done on vectors (i.e. Bloom filters); while for the other four methods, the similarity calculation was done on sets of string tokens. For each experiment for each of the six methods, the number of computational thread in Matlab was set to 1. From Table 4, it can be seen that our proposed approach has a relatively low computational cost at the intra-blocking stage. The additional pay of the proposed method on runtime is mainly in the stage of intra-blocking (i.e. handling missing values). Since the missing values in a record are handled within its own dataset, the process of handling missing values can be carried out in parallel



(a) Pair 1 (10% missing)

(b) Pair 1 (10% missing)

(c) Pair 2 (20% missing)

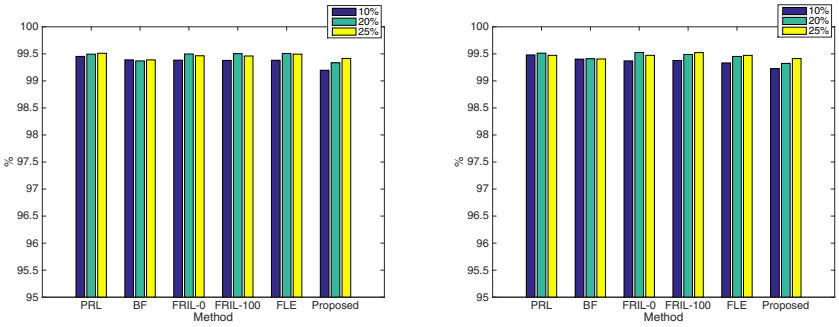
(d) Pair 2 (20% missing)

(e) Pair 3 (25% missing)

(f) Pair 3 (25% missing)

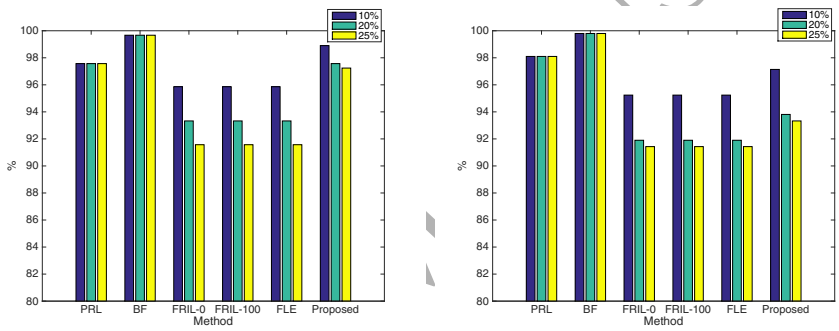
Figure 1: Comparison of linkage qualities across different methods: at most one missing value per record (the left column), and at most two missing values per record (the right column).

by each dataset owner before the process of record linkage. At the stage of blocking, both BF and our proposed approach outperform the other methods,



(a) at most one missing value per record (b) at most two missing values per record

Figure 2: Comparison of percentages of record pairs (to be matched) rejected after blocking.



(a) at most one missing value per record (b) at most two missing values per record

Figure 3: Comparison of percentages of true matches retained after blocking.

as both methods utilise Bloom filters (i.e. vectors) while Matlab works more efficiently with vectors than with string tokens. At the last stage, the linkage stage, the two methods are a little bit slower than the other methods. There are two reasons: One is that the encryption through Bloom filters are computationally quite expensive, at the linkage stage, because all the fields need to be encrypted; while at the blocking stage, only the fields used as blocking keys need to be encrypted. The other is through blocking, the number of record pairs for comparison is significantly reduced, as a result, the advantage of Matlab on computing vectors is not too obvious.

6. Conclusions

In this paper, we have proposed a new approach to privacy preserving record linkage in the presence of missing values, while at the same time addressing the scalability issue. Our approach is based on the assumption that the k-NNs of a record with a missing value in a large dataset would provide a set of similar values to the missing value, which can be used to impute the similarity measure between the record with the missing value and a record from another dataset. With the imputed similarity measures, an existing blocking technique can be directly used to deal with the scalability of record linkage. We have also adapted the Bloom filter approach so that the k-NNs of a record with a missing value can be encrypted together with the record, such that record linkage in the presence of missing values can be carried out in a privacy preserving manner. Compared with the existing algorithms for record linkage using three pairs of simulated datasets with different rates of missing values, we have shown that our proposed approach has achieved reasonably good linkage performances in the presence of missing values in a privacy preserving manner. In future work, we plan to apply the proposed approach to the real-world large-scale datasets.

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Table 2: Example of using the Bloom filter protocol to encrypt strings for computing the similarity measure between strings in a privacy preserving manner.

$h_p(\cdot)$	*SMITH*		*SMYTH*		*SMY*		*calculated*
mod l	*bit*	*bigram* (p)	*bit*	*bigram* (p)	*bit*	*bigram* (p)	*bit*
6	1	$H\_$ (3)	1	$H\_$ (3)	0		0.65
11	0		0		1	$Y\_$ (2)	0.35
12	1	SM (3)	1	SM (3)	1	SM (3)	1
13	1	MI (2)	1	MY (1)	1	MY (1)	1
17	1	IT (1)	0		0		0
21	1	$\_S$ (2)	1	$\_S$ (2)	1	$\_S$ (2)	1
32	0		1	YT (2)	0		0.65
39	0		0		1	$Y\_$ (3)	0.35
48	1	$H\_$ (1)	1	MY (2) $H\_$ (1)	1	MY (2)	1
56	1	TH (1)	1	TH (1)	0		0.65
58	1	MI (1) TH (2)	1	TH (2)	0		0.65
60	1	TH (3)	1	TH (3)	0		0.65
61	1	IT (3)	0		0		0
67	1	$\_S$ (3)	1	$\_S$ (3)	1	$\_S$ (3)	1
68	1	MI (3)	0		0		0
75	1	$\_S$ (1)	1	$\_S$ (1)	1	$\_S$ (1)	1
76	1	SM (1)	1	SM (1)	1	SM (1)	1
77	1	$H\_$ (2)	1	$H\_$ (2)	0		0.65
81	0		1	YT (3)	0		0.65
83	0		1	MY (3) YT (1)	1	MY (3) $Y\_$ (1)	1
89	1	IT (2)	0		0		0
94	1	SM (2)	1	SM (2)	1	SM (2)	1

Table 3: Characteristics of the synthetic datasets R and S

Size:	$\lvert R\rvert = 10^5$, $\lvert S\rvert = 1.05 \times 10^5$ records
Columns:	*GivenName* (GN), *Surname* (S), *Postcode* (P), *Telephone* (T), *Gender* (G), *City* (C)
Similarity:	$\mathbb{DC}(GN)$, $\mathbb{DC}(S)$, $\mathbb{DC}(P)$, $\mathbb{DC}(P, C)$ $\mathbb{DC}(T)$, $\mathbb{SE}(G)$, $\mathbb{DC}(C)$
Blocking:	$\mathbb{DC}(\text{1st of } N, S) \geq 0.7$, $\mathbb{DC}(T) \geq 0.85$
Intra-Blocking:	$\mathbb{DC}(S) \geq 0.85$, $\mathbb{DC}(P, C) \geq 0.85$, $\mathbb{DC}(T) \geq 0.85$

Table 4: Comparison of runtime at different computational stages (in hours).

Method	Computation Stage			Total
	Intra-Blocking	Blocking	Linkage	
PRL	–	14.468	1.073	15.541
BF	–	4.712	1.671	6.383
FRIL-0	–	13.523	0.946	14.469
FRIL-100	–	13.248	1.128	14.376
FLE	–	14.002	1.045	15.047
Proposed	1.526	4.902	1.913	8.341